



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Skatrud, Paul L.
Peery, Robert B.
de Waard, Maarten
- 10 (ii) TITLE OF INVENTION: Multiple Drug Resistance Gene atrD of
Aspergillus Nidulans
- (iii) NUMBER OF SEQUENCES: 3
- 15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Eli Lilly and Company
(B) STREET: Lilly Corporate Center
(C) CITY: Indianapolis
(D) STATE: Indiana
20 (E) COUNTRY: U.S.
(F) ZIP: 46285
- (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Webster, Thomas D.
(B) REGISTRATION NUMBER: 39,872
(C) REFERENCE/DOCKET NUMBER: X-11766
- (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 317-276-3334
(B) TELEFAX: 317-276-2763

(2) INFORMATION FOR SEQ ID NO:1:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4002 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- 55 (iv) ANTI-SENSE: NO
- (ix) FEATURE:
60 (A) NAME/KEY: CDS
(B) LOCATION: 1..4002
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65

X-11766

17

	ATG	TCC	CCG	CTA	GAG	ACA	AAT	CCC	CTT	TCG	CCA	GAG	ACT	GCT	ATG	CGC	48
	Met	Ser	Pro	Leu	Glu	Thr	Asn	Pro	Leu	Ser	Pro	Glu	Thr	Ala	Met	Arg	
	1				5				10						15		
5	GAA	CCT	GCT	GAG	ACT	TCA	ACG	ACG	GAG	GAG	CAA	GCT	TCT	ACA	CCA	CAC	96
	Glu	Pro	Ala	Glu	Thr	Ser	Thr	Thr	Glu	Glu	Gln	Ala	Ser	Thr	Pro	His	
				20					25					30			
10	GCT	GCG	GAC	GAG	AAG	AAA	ATC	CTC	AGC	GAC	CTC	TCG	GCT	CCA	TCT	AGT	144
	Ala	Ala	Asp	Glu	Lys	Lys	Ile	Leu	Ser	Asp	Leu	Ser	Ala	Pro	Ser	Ser	
			35					40					45				
15	ACT	ACA	GCA	ACC	CCC	GCA	GAC	AAG	GAG	CAC	CGT	CCT	AAA	TCG	TCG	TCC	192
	Thr	Thr	Ala	Thr	Pro	Ala	Ala	Lys	Glu	His	Arg	Pro	Lys	Ser	Ser	Ser	
		50						55				60					
20	AGC	AAT	AAT	GCG	GTC	TCG	GTC	AAC	GAA	GTC	GAT	GCG	CTT	ATT	GCG	CAC	240
	Ser	Asn	Asn	Ala	Val	Ser	Val	Asn	Glu	Val	Asp	Ala	Leu	Ile	Ala	His	
	65					70					75					80	
25	CTG	CCA	GAA	GAC	GAG	AGG	CAG	GTC	TTG	AAG	ACG	CAG	CTG	GAG	GAG	ATC	288
	Leu	Pro	Glu	Asp	Glu	Arg	Gln	Val	Leu	Lys	Thr	Gln	Leu	Glu	Glu	Ile	
					85					90				95			
30	AAA	GTA	AAC	ATC	TCC	TTC	TTC	GGT	CTC	TGG	CGG	TAT	GCA	ACA	AAG	ATG	336
	Lys	Val	Asn	Ile	Ser	Phe	Phe	Gly	Leu	Trp	Arg	Tyr	Ala	Thr	Lys	Met	
				100				105						110			
35	GAT	ATA	CTT	ATC	ATG	GTA	ATC	AGT	ACA	ATC	TGT	GCC	ATT	GCT	GCC	GCG	384
	Asp	Ile	Leu	Ile	Met	Val	Ile	Ser	Thr	Ile	Cys	Ala	Ile	Ala	Ala	Ala	
			115					120					125				
40	TCG	ACT	TTC	CAG	AGG	ATA	ATG	TTA	TAT	CAA	ATC	TCG	TAC	GAC	GAG	TTC	432
	Ser	Thr	Phe	Gln	Arg	Ile	Met	Leu	Tyr	Gln	Ile	Ser	Tyr	Asp	Glu	Phe	
		130					135					140					
45	TAT	GAT	GAA	TTG	ACC	AAG	AAC	GTA	CTG	TAC	TTC	GTA	TAC	CTC	GGT	ATC	480
	Tyr	Asp	Glu	Leu	Thr	Lys	Asn	Val	Leu	Tyr	Phe	Val	Tyr	Leu	Gly	Ile	
	145					150					155					160	
50	GGC	GAG	TTT	GTC	ACT	GTC	TAT	GTT	AGT	ACT	GTT	GGC	TTC	ATC	TAT	ACC	528
	Gly	Glu	Phe	Val	Thr	Val	Tyr	Val	Ser	Thr	Val	Gly	Phe	Ile	Tyr	Thr	
				165				170						175			
55	GGA	GAA	CAC	GCC	ACG	CAG	AAG	ATC	CGC	GAG	TAT	TAC	CTT	GAG	TCT	ATC	576
	Gly	Glu	His	Ala	Thr	Gln	Lys	Ile	Arg	Glu	Tyr	Tyr	Leu	Glu	Ser	Ile	
				180				185						190			
60	CTG	CGC	CAG	AAC	ATT	GGC	TAT	TTT	GAT	AAA	CTC	GGT	GCC	GGG	GAA	GTG	624
	Leu	Arg	Gln	Asn	Ile	Gly	Tyr	Phe	Asp	Lys	Leu	Gly	Ala	Gly	Glu	Val	
			195				200						205				
65	ACC	ACC	CGT	ATA	ACA	GCC	GAT	ACA	AAC	CTT	ATC	CAG	GAT	GGC	ATT	TCG	672
	Thr	Thr	Arg	Ile	Thr	Ala	Asp	Thr	Asn	Leu	Ile	Gln	Asp	Gly	Ile	Ser	
			210				215					220					
70	GAG	AAG	GTC	GGT	CTC	ACT	TTG	ACT	GCC	CTG	GCG	ACA	TTC	GTG	ACA	GCA	720
	Glu	Lys	Val	Gly	Leu	Thr	Leu	Thr	Ala	Leu	Ala	Thr	Phe	Val	Thr	Ala	
	225					230					235					240	
75	TTC	ATT	ATC	GCC	TAC	GTC	AAA	TAC	TGG	AAG	TTG	GCT	CTA	ATT	TGC	AGC	768
	Phe	Ile	Ile	Ala	Tyr	Val	Lys	Tyr	Trp	Lys	Leu	Ala	Leu	Ile	Cys	Ser	
				245						250				255			
80	TCA	ACA	ATT	GTG	GCC	CTC	GTT	CTC	ACC	ATG	GGC	GGT	GGT	TCT	CAG	TTT	816

	Ser	Thr	Ile	Val	Ala	Leu	Val	Leu	Thr	Met	Gly	Gly	Gly	Ser	Gln	Phe	
				260					265					270			
5	ATC	ATC	AAG	TAC	AGC	AAA	AAG	TCG	CTT	GAC	AGC	TAC	GGT	GCA	GGC	GGC	864
	Ile	Ile	Lys	Tyr	Ser	Lys	Lys	Ser	Leu	Asp	Ser	Tyr	Gly	Ala	Gly	Gly	
			275					280					285				
10	ACT	GTT	GCG	GAA	GAG	GTC	ATC	AGC	TCC	ATC	AGA	AAT	GCC	ACA	GCG	TTT	912
	Thr	Val	Ala	Glu	Glu	Val	Ile	Ser	Ser	Ile	Arg	Asn	Ala	Thr	Ala	Phe	
			290				295					300					
15	GGC	ACC	CAA	GAC	AAG	CTT	GCG	AAG	CAG	TAT	GAG	GTC	CAC	TTA	GAC	GAA	960
	Gly	Thr	Gln	Asp	Lys	Leu	Ala	Lys	Gln	Tyr	Glu	Val	His	Leu	Asp	Glu	
	305					310					315					320	
20	GCT	GAG	AAA	TGG	GGA	ACA	AAG	AAC	CAG	ATT	GTC	ATG	GGT	TTC	ATG	ATT	1008
	Ala	Glu	Lys	Trp	Gly	Thr	Lys	Asn	Gln	Ile	Val	Met	Gly	Phe	Met	Ile	
					325					330					335		
25	GGC	GCC	ATG	TTT	GGC	CTT	ATG	TAC	TCG	AAC	TAC	GGT	CTT	GGC	TTC	TGG	1056
	Gly	Ala	Met	Phe	Gly	Leu	Met	Tyr	Ser	Asn	Tyr	Gly	Leu	Gly	Phe	Trp	
				340					345					350			
30	ATG	GGT	TCT	CGT	TTC	CTG	GTA	GAT	GGT	GCA	GTC	GAT	GTG	GGT	GAT	ATT	1104
	Met	Gly	Ser	Arg	Phe	Leu	Val	Asp	Gly	Ala	Val	Asp	Val	Gly	Asp	Ile	
			355					360					365				
35	CTC	ACA	GTT	CTC	ATG	GCC	ATC	TTG	ATC	GGA	TCG	TTC	TCC	TTG	GGG	AAC	1152
	Leu	Thr	Val	Leu	Met	Ala	Ile	Leu	Ile	Gly	Ser	Phe	Ser	Leu	Gly	Asn	
			370				375					380					
40	GTT	AGT	CCA	AAT	GCT	CAA	GCA	TTT	ACA	AAC	GCT	GTG	GCC	GCG	GCC	GCA	1200
	Val	Ser	Pro	Asn	Ala	Gln	Ala	Phe	Thr	Asn	Ala	Val	Ala	Ala	Ala	Ala	
	385					390					395					400	
45	AAG	ATA	TTT	GGA	ACG	ATC	GAT	CGC	CAG	TCC	CCA	TTA	GAT	CCA	TAT	TCG	1248
	Lys	Ile	Phe	Gly	Thr	Ile	Asp	Arg	Gln	Ser	Pro	Leu	Asp	Pro	Tyr	Ser	
				405						410					415		
50	AAC	GAA	GGG	AAG	ACG	CTC	GAC	CAT	TTT	GAG	GGC	CAC	ATT	GAG	TTA	CGC	1296
	Asn	Glu	Gly	Lys	Thr	Leu	Asp	His	Phe	Glu	Gly	His	Ile	Glu	Leu	Arg	
				420					425					430			
55	AAT	GTC	AAG	CAT	ATT	TAC	CCA	TCT	AGA	CCC	GAG	GTC	ACC	GTC	ATG	GAG	1344
	Asn	Val	Lys	His	Ile	Tyr	Pro	Ser	Arg	Pro	Glu	Val	Thr	Val	Met	Glu	
			435					440					445				
60	GAT	GTT	TCT	CTG	TCA	ATG	CCC	GCT	GGA	AAA	ACA	ACC	GCT	TTA	GTC	GGC	1392
	Asp	Val	Ser	Leu	Ser	Met	Pro	Ala	Gly	Lys	Thr	Thr	Ala	Leu	Val	Gly	
			450				455					460					
65	CCC	TCT	GGC	TCT	GGA	AAA	AGT	ACG	GTG	GTC	GGC	TTG	GTT	GAG	CGA	TTC	1440
	Pro	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Val	Gly	Leu	Val	Glu	Arg	Phe	
	465					470					475					480	
70	TAC	ATG	CCT	GTT	CGC	GGT	ACG	GTT	TTG	CTG	GAT	GGC	CAT	GAC	ATC	AAG	1488
	Tyr	Met	Pro	Val	Arg	Gly	Thr	Val	Leu	Leu	Asp	Gly	His	Asp	Ile	Lys	
				485					490					495			
75	GAC	CTC	AAT	CTC	CGC	TGG	CTT	CGC	CAA	CAG	ATC	TCT	TTG	GTT	AGC	CAG	1536
	Asp	Leu	Asn	Leu	Arg	Trp	Leu	Arg	Gln	Gln	Ile	Ser	Leu	Val	Ser	Gln	
				500				505						510			
80	GAG	CCT	GTT	CTT	TTT	GGC	ACG	ACG	ATT	TAT	AAG	AAT	ATT	AGG	CAC	GGT	1584
	Glu	Pro	Val	Leu	Phe	Gly	Thr	Thr	Ile	Tyr	Lys	Asn	Ile	Arg	His	Gly	

19

	515							520							525							
5	CTC Leu	ATC Ile	GGC Gly	ACA Thr	AAG Lys	TAC Tyr	GAG Glu	AAT Asn	GAA Glu	TCC Ser	GAG Glu	GAT Asp	AAG Lys	GTC Val	CGG Arg	GAA Glu	1632					
	530						535					540										
10	CTC Leu	ATC Ile	GAG Glu	AAC Asn	GCG Ala	GCA Ala	AAA Lys	ATG Met	GCG Ala	AAT Asn	GCT Ala	CAT His	GAC Asp	TTT Phe	ATT Ile	ACT Thr	1680					
	545					550					555					560						
15	GCC Ala	TTG Leu	CCT Pro	GAA Glu	GGT Gly	TAT Tyr	GAG Glu	ACC Thr	AAT Asn	GTT Val	GGG Gly	CAG Gln	CGT Arg	GGC Gly	TTT Phe	CTC Leu	1728					
					565					570					575							
20	CTT Leu	TCA Ser	GGT Gly	GGC Gly	CAG Gln	AAA Lys	CAG Gln	CGC Arg	ATT Ile	GCA Ala	ATC Ile	GCC Ala	CGT Arg	GCC Ala	GTT Val	GTT Val	1776					
				580					585					590								
25	AGT Ser	GAC Asp	CCA Pro	AAA Lys	ATC Ile	CTG Leu	CTC Leu	CTG Leu	GAT Asp	GAA Glu	GCT Ala	ACT Thr	TCG Ser	GCC Ala	TTG Leu	GAC Asp	1824					
			595					600					605									
30	ACA Thr	AAA Lys	TCC Ser	GAA Glu	GGC Gly	GTG Val	GTT Val	CAA Gln	GCA Ala	GCT Ala	TTG Leu	GAG Glu	AGG Arg	GCA Ala	GCT Ala	GAA Glu	1872					
	610						615					620										
35	GGC Gly	CGA Arg	ACT Thr	ACT Thr	ATT Ile	GTG Val	ATC Ile	GCT Ala	CAT His	CGC Arg	CTT Leu	TCC Ser	ACG Thr	ATC Ile	AAA Lys	ACG Thr	1920					
	625					630					635					640						
40	GCG Ala	CAC His	AAC Asn	ATT Ile	GTG Val	GTT Val	CTG Leu	GTC Val	AAT Asn	GGC Gly	AAA Lys	ATT Ile	GCT Ala	GAA Glu	CAA Gln	GGA Gly	1968					
					645					650					655							
45	ACT Thr	CAC His	GAT Asp	GAA Glu	TTG Leu	GTT Val	GAC Asp	CGC Arg	GGA Gly	GGC Gly	GCT Ala	TAT Tyr	CGC Arg	AAA Lys	CTT Leu	GTG Val	2016					
				660					665					670								
50	GAG Glu	GCT Ala	CAA Gln	CGT Arg	ATC Ile	AAT Asn	GAA Glu	CAG Gln	AAG Lys	GAA Glu	GCT Ala	GAC Asp	GCC Ala	TTG Leu	GAG Glu	GAC Asp	2064					
			675					680					685									
55	GCC Ala	GAC Asp	GCT Ala	GAG Glu	GAT Asp	CTC Leu	ACG Thr	AAT Asn	GCA Ala	GAT Asp	ATT Ile	GCC Ala	AAA Lys	ATC Ile	AAA Lys	ACT Thr	2112					
	690						695					700										
60	GCG Ala	TCA Ser	AGC Ser	GCA Ala	TCA Ser	TCC Ser	GAT Asp	CTC Leu	GAC Asp	GGA Gly	AAA Lys	CCC Pro	ACA Thr	ACC Thr	ATT Ile	GAC Asp	2160					
	705					710					715					720						
65	CGC Arg	ACG Thr	GGC Gly	ACC Thr	CAC His	AAG Lys	TCT Ser	GTT Val	TCC Ser	AGC Ser	GCG Ala	ATT Ile	CTT Leu	TCT Ser	AAA Lys	AGA Arg	2208					
					725				730						735							
70	CCC Pro	CCC Pro	GAA Glu	ACA Thr	ACT Thr	CCG Pro	AAA Lys	TAC Tyr	TCA Ser	TTA Leu	TGG Trp	ACG Thr	CTG Leu	CTC Leu	AAA Lys	TTT Phe	2256					
			740					745					750									
75	GTT Val	GCT Ala	TCC Ser	TTC Phe	AAC Asn	CGC Arg	CCT Pro	GAA Glu	ATC Ile	CCG Pro	TAC Tyr	ATG Met	CTC Leu	ATC Ile	GGT Gly	CTT Leu	2304					
			755					760					765									
80	GTC Val	TTC Phe	TCA Ser	GTG Val	TTA Leu	GCT Ala	GGT Gly	GGT Gly	GGC Gly	CAA Gln	CCC Pro	ACG Thr	CAA Gln	GCA Ala	GTG Val	CTA Leu	2352					
		770					775					780										

20

5	TAT Tyr 785	GCT Ala	AAA Lys	GCC Ala	ATC Ile	AGC Ser 790	ACA Thr	CTC Leu	TCG Ser	CTC Leu	CCA Pro 795	GAA Glu	TCA Ser	CAA Gln	TAT Tyr	AGC Ser 800	2400
	AAG Lys	CTT Leu	CGA Arg	CAT His	GAT Asp 805	GCG Ala	GAT Asp	TTC Phe	TGG Trp	TCA Ser 810	TTG Leu	ATG Met	TTC Phe	TTC Phe	GTG Val 815	GTT Val	2448
10	GGT Gly	ATC Ile	ATT Ile	CAG Gln 820	TTT Phe	ATC Ile	ACG Thr	CAG Gln	TCA Ser 825	ACC Thr	AAT Asn	GGT Gly	GCT Ala	GCA Ala 830	TTT Phe	GCC Ala	2496
15	GTA Val	TGC Cys	TCC Ser 835	GAG Glu	AGA Arg	CTT Leu	ATT Ile	CGT Arg 840	CGC Arg	GCG Ala	AGA Arg	AGC Ser	ACT Thr 845	GCC Ala	TTT Phe	CGG Arg	2544
20	ACG Thr 850	ATA Ile	CTC Leu	CGT Arg	CAA Gln	GAC Asp	ATT Ile 855	GCT Ala	TTC Phe	TTT Phe	GAC Asp	AAG Lys 860	GAA Glu	GAG Glu	AAT Asn	AGC Ser	2592
	ACC Thr 865	GGC Gly	GCT Ala	CTG Leu	ACC Thr	TCT Ser 870	TTC Phe	CTG Leu	TCC Ser	ACC Thr	GAG Glu 875	ACG Thr	AAG Lys	CAT His	CTC Leu	TCC Ser 880	2640
25	GGT Gly	GTT Val	AGC Ser	GGT Gly	GTG Val 885	ACT Thr	CTA Leu	GGC Gly	ACG Thr	ATC Ile 890	TTG Leu	ATG Met	ACC Thr	TCC Ser	ACG Thr 895	ACC Thr	2688
30	CTA Leu	GGA Gly	GCG Ala	GCT Ala 900	ATC Ile	ATT Ile	ATT Ile	GCC Ala	CTG Leu 905	GCG Ala	ATT Ile	GGG Gly	TGG Trp	AAA Lys 910	TTG Leu	GCC Ala	2736
35	TTA Leu	GTT Val	TGT Cys 915	ATC Ile	TCG Ser	GTT Val	GTG Val	CCG Pro 920	GTT Val	CTC Leu	CTG Leu	GCA Ala	TGC Cys 925	GGT Gly	TTC Phe	TAC Tyr	2784
40	CGA Arg 930	TTC Phe	TAT Tyr	ATG Met	CTA Leu	GCC Ala	CAG Gln 935	TTT Phe	CAA Gln	TCA Ser	CGC Arg	TCC Ser 940	AAG Lys	CTT Leu	GCT Ala	TAT Tyr	2832
45	GAG Glu 945	GGA Gly	TCT Ser	GCA Ala	AAC Asn 950	TTT Phe	GCT Ala	TGC Cys	GAG Glu	GCT Ala	ACA Thr 955	TCG Ser	TCT Ser	ATC Ile	CGC Arg	ACA Thr 960	2880
	GTT Val	GCG Ala	TCA Ser	TTA Leu	ACC Thr 965	CGG Arg	GAA Glu	AGG Arg	GAT Asp	GTC Val 970	TGG Trp	GAG Glu	ATT Ile	TAC Tyr	CAT His 975	GCC Ala	2928
50	CAG Gln	CTT Leu	GAC Asp	GCA Ala 980	CAA Gln	GGC Gly	AGG Arg	ACC Thr	AGT Ser 985	CTA Leu	ATC Ile	TCT Ser	GTC Val	TTG Leu 990	AGG Arg	TCA Ser	2976
55	TCC Ser	CTG Leu	TTA Leu 995	TAT Tyr	GCG Ala	TCG Ser	TCG Ser	CAG Gln 1000	GCA Ala	CTT Leu	GTT Val	TTC Phe	TTC Phe 1005	TGC Cys	GTT Val	GCG Ala	3024
60	CTC Leu 1010	GGG Gly	TTT Phe	TGG Trp	TAC Tyr	GGA Gly	GGG Gly 1015	ACA Thr	CTT Leu	CTT Leu	GGT Gly	CAC His 1020	CAC His	GAG Glu	TAT Tyr	GAC Asp	3072
65	ATT Ile 1025	TTC Phe	CGC Arg	TTC Phe	TTT Phe	GTT Val 1030	TGT Cys	TTC Phe	TCC Ser	GAG Glu	ATT Ile 1035	CTC Leu	TTT Phe	GGT Gly	GCT Ala	CAA Gln 1040	3120

21

	TCC	GCG	GGC	ACC	GTC	TTT	TCC	TTT	GCA	CCA	GAC	ATG	GGC	AAG	GCG	AAG	3168
	Ser	Ala	Gly	Thr	Val	Phe	Ser	Phe	Ala	Pro	Asp	Met	Gly	Lys	Ala	Lys	
					1045					1050						1055	
5	AAT	GCG	GCC	GCC	GAA	TTC	CGA	CGA	CTG	TTC	GAC	CGA	AAG	CCA	CAA	ATT	3216
	Asn	Ala	Ala	Ala	Glu	Phe	Arg	Arg	Leu	Phe	Asp	Arg	Lys	Pro	Gln	Ile	
					1060					1065						1070	
10	GAT	AAC	TGG	TCT	GAA	GAG	GGC	GAG	AAG	CTC	GAA	ACG	GTG	GAA	GGT	GAA	3264
	Asp	Asn	Trp	Ser	Glu	Glu	Gly	Glu	Lys	Leu	Glu	Thr	Val	Glu	Gly	Glu	
					1075					1080						1085	
15	ATC	GAA	TTT	AGG	AAC	GTG	CAC	TTC	AGA	TAC	CCG	ACC	CGC	CCA	GAA	CAG	3312
	Ile	Glu	Phe	Arg	Asn	Val	His	Phe	Arg	Tyr	Pro	Thr	Arg	Pro	Glu	Gln	
					1090					1095						1100	
20	CCT	GTC	CTG	CGC	GGC	TTG	GAC	CTG	ACC	GTG	AAG	CCT	GGA	CAA	TAT	GTT	3360
	Pro	Val	Leu	Arg	Gly	Leu	Asp	Leu	Thr	Val	Lys	Pro	Gly	Gln	Tyr	Val	
					1105											1120	
25	GCG	CTT	GTC	GGA	CCC	AGC	GGT	TGT	GGC	AAG	AGT	ACC	ACC	ATT	GCA	TTG	3408
	Ala	Leu	Val	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Thr	Ile	Ala	Leu	
					1125											1135	
30	CTT	GAG	CGC	TTT	TAC	GAT	GCG	ATT	GCC	GGG	TCC	ATC	CTT	GTT	GAT	GGG	3456
	Leu	Glu	Arg	Phe	Tyr	Asp	Ala	Ile	Ala	Gly	Ser	Ile	Leu	Val	Asp	Gly	
					1140											1150	
35	AAG	GAC	ATA	AGT	AAA	CTA	AAT	ATC	AAC	TCC	TAC	CGC	AGC	TTT	CTG	TCA	3504
	Lys	Asp	Ile	Ser	Lys	Leu	Asn	Ile	Asn	Ser	Tyr	Arg	Ser	Phe	Leu	Ser	
					1155											1165	
40	CTG	GTC	AGC	CAG	GAG	CCG	ACA	CTG	TAC	CAG	GGC	ACC	ATC	AAG	GAA	AAC	3552
	Leu	Val	Ser	Gln	Glu	Pro	Thr	Leu	Tyr	Gln	Gly	Thr	Ile	Lys	Glu	Asn	
					1170											1180	
45	ATC	TTA	CTT	GGT	ATT	GTC	GAA	GAT	GAC	GTA	CCG	GAA	GAA	TTC	TTG	ATT	3600
	Ile	Leu	Leu	Gly	Ile	Val	Glu	Asp	Asp	Val	Pro	Glu	Glu	Phe	Leu	Ile	
					1185											1200	
50	AAG	GCT	TGC	AAG	GAC	GCT	AAT	ATC	TAC	GAC	TTC	ATC	ATG	TCG	CTC	CCG	3648
	Lys	Ala	Cys	Lys	Asp	Ala	Asn	Ile	Tyr	Asp	Phe	Ile	Met	Ser	Leu	Pro	
					1205											1215	
55	GAG	GGC	TTT	AAT	ACA	GTT	GTT	GGC	AGC	AAG	GGA	GGC	ATG	TTG	TCT	GGC	3696
	Glu	Gly	Phe	Asn	Thr	Val	Val	Gly	Ser	Lys	Gly	Gly	Met	Leu	Ser	Gly	
					1220											1230	
60	GGC	CAA	AAG	CAA	CGT	GTG	GCC	ATT	GCC	CGA	GCC	CTT	CTT	CGG	GAT	CCC	3744
	Gly	Gln	Lys	Gln													

X-11766

22

Ile Tyr Val Phe Asp Gln Gly Lys Ile Val Glu Ser Gly Thr His Ser
1300 1305 1310

5 GAA CTG GTC CAG AAA AAG GGC CGG TAC TAC GAG CTG GTC AAC TTG CAG 3984
Glu Leu Val Gln Lys Lys Gly Arg Tyr Tyr Glu Leu Val Asn Leu Gln
1315 1320 1325

AGC TTG GGC AAG GGC CAT 4002
Ser Leu Gly Lys Gly His
1330

(2) INFORMATION FOR SEQ ID NO:2:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1334 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Ser Pro Leu Glu Thr Asn Pro Leu Ser Pro Glu Thr Ala Met Arg
1 5 10 15

Glu Pro Ala Glu Thr Ser Thr Thr Glu Glu Gln Ala Ser Thr Pro His
20 25 30

30 Ala Ala Asp Glu Lys Lys Ile Leu Ser Asp Leu Ser Ala Pro Ser Ser
35 40 45

Thr Thr Ala Thr Pro Ala Asp Lys Glu His Arg Pro Lys Ser Ser Ser
50 55 60

35 Ser Asn Asn Ala Val Ser Val Asn Glu Val Asp Ala Leu Ile Ala His
65 70 75 80

40 Leu Pro Glu Asp Glu Arg Gln Val Leu Lys Thr Gln Leu Glu Glu Ile
85 90 95

Lys Val Asn Ile Ser Phe Phe Gly Leu Trp Arg Tyr Ala Thr Lys Met
100 105 110

45 Asp Ile Leu Ile Met Val Ile Ser Thr Ile Cys Ala Ile Ala Ala Ala
115 120 125

Ser Thr Phe Gln Arg Ile Met Leu Tyr Gln Ile Ser Tyr Asp Glu Phe
130 135 140

50 Tyr Asp Glu Leu Thr Lys Asn Val Leu Tyr Phe Val Tyr Leu Gly Ile
145 150 155 160

55 Gly Glu Phe Val Thr Val Tyr Val Ser Thr Val Gly Phe Ile Tyr Thr
165 170 175

Gly Glu His Ala Thr Gln Lys Ile Arg Glu Tyr Tyr Leu Glu Ser Ile
180 185 190

60 Leu Arg Gln Asn Ile Gly Tyr Phe Asp Lys Leu Gly Ala Gly Glu Val
195 200 205

Thr Thr Arg Ile Thr Ala Asp Thr Asn Leu Ile Gln Asp Gly Ile Ser
210 215 220

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	Glu	Lys	Val	Gly	Leu	Thr	Leu	Thr	Ala	Leu	Ala	Thr	Phe	Val	Thr	Ala
	225						230				235					240
5	Phe	Ile	Ile	Ala	Tyr	Val	Lys	Tyr	Trp	Lys	Leu	Ala	Leu	Ile	Cys	Ser
					245					250					255	
	Ser	Thr	Ile	Val	Ala	Leu	Val	Leu	Thr	Met	Gly	Gly	Gly	Ser	Gln	Phe
				260					265					270		
10	Ile	Ile	Lys	Tyr	Ser	Lys	Lys	Ser	Leu	Asp	Ser	Tyr	Gly	Ala	Gly	Gly
			275					280					285			
	Thr	Val	Ala	Glu	Glu	Val	Ile	Ser	Ser	Ile	Arg	Asn	Ala	Thr	Ala	Phe
	290						295					300				
15	Gly	Thr	Gln	Asp	Lys	Leu	Ala	Lys	Gln	Tyr	Glu	Val	His	Leu	Asp	Glu
	305					310					315					320
	Ala	Glu	Lys	Trp	Gly	Thr	Lys	Asn	Gln	Ile	Val	Met	Gly	Phe	Met	Ile
					325					330					335	
20	Gly	Ala	Met	Phe	Gly	Leu	Met	Tyr	Ser	Asn	Tyr	Gly	Leu	Gly	Phe	Trp
				340					345					350		
25	Met	Gly	Ser	Arg	Phe	Leu	Val	Asp	Gly	Ala	Val	Asp	Val	Gly	Asp	Ile
			355					360					365			
	Leu	Thr	Val	Leu	Met	Ala	Ile	Leu	Ile	Gly	Ser	Phe	Ser	Leu	Gly	Asn
	370						375					380				
30	Val	Ser	Pro	Asn	Ala	Gln	Ala	Phe	Thr	Asn	Ala	Val	Ala	Ala	Ala	Ala
	385					390					395					400
	Lys	Ile	Phe	Gly	Thr	Ile	Asp	Arg	Gln	Ser	Pro	Leu	Asp	Pro	Tyr	Ser
					405					410					415	
35	Asn	Glu	Gly	Lys	Thr	Leu	Asp	His	Phe	Glu	Gly	His	Ile	Glu	Leu	Arg
				420					425					430		
40	Asn	Val	Lys	His	Ile	Tyr	Pro	Ser	Arg	Pro	Glu	Val	Thr	Val	Met	Glu
			435					440					445			
	Asp	Val	Ser	Leu	Ser	Met	Pro	Ala	Gly	Lys	Thr	Thr	Ala	Leu	Val	Gly
	450						455					460				
45	Pro	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Val	Gly	Leu	Val	Glu	Arg	Phe
	465					470					475					480
	Tyr	Met	Pro	Val	Arg	Gly	Thr	Val	Leu	Leu	Asp	Gly	His	Asp	Ile	Lys
					485					490					495	
50	Asp	Leu	Asn	Leu	Arg	Trp	Leu	Arg	Gln	Gln	Ile	Ser	Leu	Val	Ser	Gln
				500					505					510		
55	Glu	Pro	Val	Leu	Phe	Gly	Thr	Thr	Ile	Tyr	Lys	Asn	Ile	Arg	His	Gly
			515					520					525			
	Leu	Ile	Gly	Thr	Lys	Tyr	Glu	Asn	Glu	Ser	Glu	Asp	Lys	Val	Arg	Glu
	530						535					540				
60	Leu	Ile	Glu	Asn	Ala	Ala	Lys	Met	Ala	Asn	Ala	His	Asp	Phe	Ile	Thr
	545					550										

	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg	Ile	Ala	Ile	Ala	Arg	Ala	Val	Val
				580					585						590	
5	Ser	Asp	Pro	Lys	Ile	Leu	Leu	Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp
			595					600					605			
	Thr	Lys	Ser	Glu	Gly	Val	Val	Gln	Ala	Ala	Leu	Glu	Arg	Ala	Ala	Glu
		610					615					620				
10	Gly	Arg	Thr	Thr	Ile	Val	Ile	Ala	His	Arg	Leu	Ser	Thr	Ile	Lys	Thr
		625				630					635					640
	Ala	His	Asn	Ile	Val	Val	Leu	Val	Asn	Gly	Lys	Ile	Ala	Glu	Gln	Gly
					645					650					655	
15	Thr	His	Asp	Glu	Leu	Val	Asp	Arg	Gly	Gly	Ala	Tyr	Arg	Lys	Leu	Val
				660					665					670		
20	Glu	Ala	Gln	Arg	Ile	Asn	Glu	Gln	Lys	Glu	Ala	Asp	Ala	Leu	Glu	Asp
			675					680					685			
	Ala	Asp	Ala	Glu	Asp	Leu	Thr	Asn	Ala	Asp	Ile	Ala	Lys	Ile	Lys	Thr
		690					695					700				
25	Ala	Ser	Ser	Ala	Ser	Ser	Asp	Leu	Asp	Gly	Lys	Pro	Thr	Thr	Ile	Asp
		705					710				715					720
	Arg	Thr	Gly	Thr	His	Lys	Ser	Val	Ser	Ser	Ala	Ile	Leu	Ser	Lys	Arg
					725					730					735	
30	Pro	Pro	Glu	Thr	Thr	Pro	Lys	Tyr	Ser	Leu	Trp	Thr	Leu	Leu	Lys	Phe
				740					745					750		
35	Val	Ala	Ser	Phe	Asn	Arg	Pro	Glu	Ile	Pro	Tyr	Met	Leu	Ile	Gly	Leu
			755					760					765			
	Val	Phe	Ser	Val	Leu	Ala	Gly	Gly	Gly	Gln	Pro	Thr	Gln	Ala	Val	Leu
		770					775					780				
40	Tyr	Ala	Lys	Ala	Ile	Ser	Thr	Leu	Ser	Leu	Pro	Glu	Ser	Gln	Tyr	Ser
		785				790					795					800
	Lys	Leu	Arg	His	Asp	Ala	Asp	Phe	Trp	Ser	Leu	Met	Phe	Phe	Val	Val
					805					810					815	
	Gly	Ile	Ile	Gln	Phe	Ile	Thr	Gln	Ser	Thr	Asn	Gly	Ala	Ala	Phe	Ala
				820					825					830		
50	Val	Cys	Ser	Glu	Arg	Leu	Ile	Arg	Arg	Ala	Arg	Ser	Thr	Ala	Phe	Arg
			835					840					845			
	Thr	Ile	Leu	Arg	Gln	Asp	Ile	Ala	Phe	Phe	Asp	Lys	Glu	Glu	Asn	Ser
		850				855						860				
55	Thr	Gly	Ala	Leu	Thr	Ser	Phe	Leu	Ser	Thr	Glu	Thr	Lys	His	Leu	Ser
		865				870					875					880
	Gly	Val	Ser	Gly	Val	Thr	Leu	Gly	Thr	Ile	Leu	Met	Thr	Ser	Thr	Thr
					885					890					895	
60	Leu	Gly	Ala	Ala	Ile	Ile	Ile	Ala	Leu	Ala	Ile	Gly	Trp	Lys	Leu	Ala
				900					905					910		
65	Leu	Val	Cys	Ile	Ser	Val	Val	Pro	Val	Leu	Leu	Ala	Cys	Gly	Phe	Tyr

X-11766

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	915					920					925					
	Arg	Phe	Tyr	Met	Leu	Ala	Gln	Phe	Gln	Ser	Arg	Ser	Lys	Leu	Ala	Tyr
		930					935					940				
5	Glu	Gly	Ser	Ala	Asn	Phe	Ala	Cys	Glu	Ala	Thr	Ser	Ser	Ile	Arg	Thr
	945				950						955					960
	Val	Ala	Ser	Leu	Thr	Arg	Glu	Arg	Asp	Val	Trp	Glu	Ile	Tyr	His	Ala
10					965					970					975	
	Gln	Leu	Asp	Ala	Gln	Gly	Arg	Thr	Ser	Leu	Ile	Ser	Val	Leu	Arg	Ser
				980					985					990		
15	Ser	Leu	Leu	Tyr	Ala	Ser	Ser	Gln	Ala	Leu	Val	Phe	Phe	Cys	Val	Ala
			995					1000					1005			
	Leu	Gly	Phe	Trp	Tyr	Gly	Gly	Thr	Leu	Leu	Gly	His	His	Glu	Tyr	Asp
20		1010					1015					1020				
	Ile	Phe	Arg	Phe	Phe	Val	Cys	Phe	Ser	Glu	Ile	Leu	Phe	Gly	Ala	Gln
	1025				1030						1035					1040
25	Ser	Ala	Gly	Thr	Val	Phe	Ser	Phe	Ala	Pro	Asp	Met	Gly	Lys	Ala	Lys
				1045						1050					1055	
	Asn	Ala	Ala	Ala	Glu	Phe	Arg	Arg	Leu	Phe	Asp	Arg	Lys	Pro	Gln	Ile
				1060					1065					1070		
30	Asp	Asn	Trp	Ser	Glu	Glu	Gly	Glu	Lys	Leu	Glu	Thr	Val	Glu	Gly	Glu
			1075					1080					1085			
	Ile	Glu	Phe	Arg	Asn	Val	His	Phe	Arg	Tyr	Pro	Thr	Arg	Pro	Glu	Gln
35		1090					1095					1100				
	Pro	Val	Leu	Arg	Gly	Leu	Asp	Leu	Thr	Val	Lys	Pro	Gly	Gln	Tyr	Val
	1105				1110						1115					1120
40	Ala	Leu	Val	Gly	Pro	Ser	Gly	Cys	Gly	Lys	Ser	Thr	Thr	Ile	Ala	Leu
				1125						1130					1135	
	Leu	Glu	Arg	Phe	Tyr	Asp	Ala	Ile	Ala	Gly	Ser	Ile	Leu	Val	Asp	Gly
				1140				1145						1150		
45	Lys	Asp	Ile	Ser	Lys	Leu	Asn	Ile	Asn	Ser	Tyr	Arg	Ser	Phe	Leu	Ser
		1155						1160					1165			
	Leu	Val	Ser	Gln	Glu	Pro	Thr	Leu	Tyr	Gln	Gly	Thr	Ile	Lys	Glu	Asn
		1170					1175					1180				
50	Ile	Leu	Leu	Gly	Ile	Val	Glu	Asp	Asp	Val	Pro	Glu	Glu	Phe	Leu	Ile
	1185				1190						1195					1200
55	Lys	Ala	Cys	Lys	Asp	Ala	Asn	Ile	Tyr	Asp	Phe	Ile	Met	Ser	Leu	Pro
				1205						1210					1215	
	Glu	Gly	Phe	Asn	Thr	Val	Val	Gly	Ser	Lys	Gly	Gly	Met	Leu	Ser	Gly
				1220					1225					1230		
60	Gly	Gln	Lys	Gln	Arg	Val	Ala	Ile	Ala	Arg	Ala	Leu	Leu	Arg	Asp	Pro
			1235					1240						1245		
	Lys	Ile	Leu	Leu	Leu	Asp	Glu	Ala	Thr	Ser	Ala	Leu	Asp	Ser	Glu	Ser
65		1250					1255						1260			

X-11766

26

Glu Lys Val Val Gln Ala Ala Leu Asp Ala Ala Ala Arg Gly Arg Thr
1265 1270 1275 1280

5 Thr Ile Ala Val Ala His Arg Leu Ser Thr Ile Gln Lys Ala Asp Val
1285 1290 1295

Ile Tyr Val Phe Asp Gln Gly Lys Ile Val Glu Ser Gly Thr His Ser
1300 1305 1310

10 Glu Leu Val Gln Lys Lys Gly Arg Tyr Tyr Glu Leu Val Asn Leu Gln
1315 1320 1325

Ser Leu Gly Lys Gly His
1330

15 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 4002 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

35 AUGUCCCCGC UAGAGACAAA UCCCCUUCG CCAGAGACUG CUAUGCGCGA ACCUGCUGAG 60
ACUUAACGA CGGAGGAGCA AGCUUCUACA CCACACGCUG CGGACGAGAA GAAAAUCCUC 120
AGCGACCUCU CGGCUCCAUC UAGUACUACA GCAACCCCGG CAGACAAGGA GCACCGUCCU 180
40 AAAUCGUUGU CCAGCAUAA UGCGGUCUCG GUCAACGAAG UCGAUGCGCU UAUUGCGCAC 240
CUGCCAGAAG ACGAGAGGCA GGUCUUGAAG ACGCAGCUGG AGGAGAUCAA AGUAAACAUC 300
45 UCCUUCUUCG GUCUCUGGCG GUAUGCAACA AAGAUGGAUA UACUUAUCAU GGUAUUCAGU 360
ACAAUCUGUG CCAUUGCUGC CGCGUCGACU UCCAGAGGA UAAUGUUAUA UCAAAUCUCG 420
UACGACGAGU UCUAUGAUGA AUUGACCAAG AACGUACUGU ACUUCGUUAU CCUCGGUAUC 480
50 GCGGAGUUUG UCACUGUCUA UGUUAGUACU GUUGGCUUCA UCUAUACCGG AGAACACGCC 540
ACGCAGAAGA UCCGCGAGUA UUACCUUGAG UCUAUCCUGC GCCAGAACAU UGGCUAUUUU 600
55 GAUAAACUCG GUGCCGGGGA AGUGACCACC CGUAUAACAG CCGAUACAAA CCUUAUCCAG 660
GAUGGCAUUU CGGAGAAGGU CGGUCUCACU UUGACUGCCC UGGCGACAUU CGUGACAGCA 720
UUCAUUAUCG CCUACGUCAA AUACUGGAAG UUGGCUCUAA UUUGCAGCUC AACAAUUGUG 780
60 GCCCUCGUUC UCACCAUGGG CGGUGGUUCU CAGUUUAUCA UCAAGUACAG CAAAAGUCG 840
CUUGACAGCU ACGGUGCAGG CGGCACUGUU GCGGAAGAGG UCAUCAGCUC CAUCAGAAAU 900
65 GCCACAGCGU UUGGCACCCA AGACAAGCUU GCGAAGCAGU AUGAGGUCCA CUUAGACGAA 960

	GCUGAGAAAU	GGGGAACAAA	GAACCAGAUU	GUCAUGGGUU	UCAUGAUUGG	CGCCAUGUUU	1020
5	GGCCUUAUGU	ACUCGAACUA	CGGUCUUGGC	UUCUGGAUGG	GUUCUCGUUU	CCUGGUAGAU	1080
	GGUGCAGUCG	AUGUGGGUGA	UAUUCUCACA	GUUCUCAUGG	CCAUCUUGAU	CGGAUCGUUC	1140
	UCCUUGGGGA	ACGUUAGUCC	AAAUGCUCAA	GCAUUUACAA	ACGCUGUGGC	CGCGGCCGCA	1200
10	AAGAUUUUG	GAACGAUCGA	UCGCCAGUCC	CCAUUAGAUC	CAUAUUCGAA	CGAAGGGAAG	1260
	ACGCUCGACC	AUUUUGAGGG	CCACAUUGAG	UUACGCAAUG	UCAAGCAUUA	UUACCCAUUCU	1320
15	AGACCCGAGG	UCACCGUCAU	GGAGGAUGUU	UCUCUGUCAA	UGCCCGCUGG	AAAAACAACC	1380
	GCUUUAGUCG	GCCCCUCUGG	CUCUGGAAAA	AGUACGGUGG	UCGGCUUGGU	UGAGCGAUUC	1440
	UACAUGCCUG	UUCGCGGUAC	GGUUUUGCUG	GAUGGCCAUG	ACAUCAAGGA	CCUCAAUUCUC	1500
20	CGCUGGCUUC	GCCAACAGAU	CUCUUUGGUU	AGCCAGGAGC	CUGUUCUUUU	UGGCACGACG	1560
	AUUUAUAAGA	AUAUUAGGCA	CGGUCUCAUC	GGCACAAAGU	ACGAGAAUGA	AUCCGAGGAU	1620
25	AAGGUCCGGG	AACUCAUCGA	GAACGCGGCA	AAAAUGGCGA	AUGCUCAUUA	CUUUUUUACU	1680
	GCCUUGCCUG	AAGGUUAUGA	GACCAAUGUU	GGGAGCGUGG	GCUUUCUCCU	UUCAGGUGGC	1740
	CAGAAACAGC	GCAUUGCAAU	CGCCCUGUGCC	GUUGUUAGUG	ACCCAAAAAU	CCUGCUCCUG	1800
30	GAUGAAGCUA	CUUCGGCCUU	GGACACAAAA	UCCGAAGGCG	UGGUUCAAGC	AGCUUUGGAG	1860
	AGGGCAGCUG	AAGGCCGAAC	UACUAUUGUG	AUCGCUCAUC	GCCUUUCCAC	GAUCAAACG	1920
35	GCGCACAACA	UUGUGGUUCU	GGUCAUUGGC	AAAAUUGCUG	AACAAGGAAC	UCACGAUGAA	1980
	UUGGUUGACC	GCGGAGGCGC	UUANCGCAA	CUUGUGGAGG	CUCAACGUUA	CAAUGAACAG	2040
	AAGGAAGCUG	ACGCCUUGGA	GGACGCCGAC	GCUGAGGAUC	UCACGAAUGC	AGAUUUGCC	2100
40	AAAUAUAAA	CUGCGUCAAG	CGCAUCAUCC	GAUCUCGACG	GAAAACCCAC	AACCAUUGAC	2160
	CGCACGGGCA	CCCACAAGUC	UGUUUCCAGC	GCGAUUCUUU	CUAAAAGACC	CCCCGAAACA	2220
45	ACUCCGAAAU	ACUCAUUAUG	GACGCUGCUC	AAAUUUGUUG	CUUCCUUCAA	CCGCCUGAA	2280
	AUCCCGUACA	UGCUCAUCCG	UCUUGUCUUC	UCAGUGUUAG	CUGGUGGUGG	CCAACCCACG	2340
	CAAGCAGUGC	UAUAUGCUAA	AGCCAUCAGC	ACACUCUCGC	UCCCAGAAUC	ACAAUAUAGC	2400
50	AAGCUUCGAC	AUGAUGCAGA	UUUCUGGUCA	UUGAUGUUCU	UCGUGGUUGG	UAUCAUUCAG	2460
	UUUAUCACGC	AGUCAACCAA	UGGUGCUGCA	UUUGCCGUUA	GCUCCGAGAG	ACUUAUUCGU	2520
55	CGCGCGAGAA	GCACUGCCUU	UCGGACGAUA	CUCCGUCAAG	ACAUUGCUTU	CUUUGACAAG	2580
	GAAGAGAAUA	GCACCGGCGC	UCUGACCUCU	UUCCUGUCCA	CCGAGACGAA	GCAUCUCUCC	2640
	GGUGUUAGCG	GUGUGACUCU	AGGCACGAUC	UUGAUGACCU	CCACGACCCU	AGGAGCGGCU	2700
60	AUCAUUAUUG	CCCUGGCGAU	UGGGUGGAAA	UUGGCCUUAG	UUUGUAUCUC	GGUUGUGCCG	2760
	GUUCUCCUGG	CAUGCAGUUU	CUACCGAUUC	UAUAUGCUAG	CCCAGUUUCA	AUCACGCUCC	2820
65	AAGCUUGCUU	AUGAGGGAUC	UGCAAACUUU	GCUUGCGAGG	CUACAUCGUC	UAUCCGCACA	2880

[illegible]

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